

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Alderson, Mark R.  
Goodwin, Raymond G.  
Smith, Craig A.
- (ii) TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand And  
Human Receptor That Binds Thereto
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation
  - (B) STREET: 51 University Street
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: US
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seese, Kathryn A.
  - (B) REGISTRATION NUMBER: 32,172
  - (C) REFERENCE/DOCKET NUMBER: 2801-WO
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 587-0430
  - (B) TELEFAX: (206) 233-0644

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: murine 4-1BB-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 53..979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: *Protein, L*

AGCCTATAAA GCACGGGCAC TGGCGGGAGA CGTGCACTGA CCGACCGTGG TA ATG	55
Met	
1	
GAC CAG CAC ACA CTT GAT GTG GAG GAT ACC GCG GAT GCC AGA CAT CCA	103
Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His Pro	
5 10 15	
GCA GGT ACT TCG TGC CCC TCG GAT GCG GCG CTC CTC AGA GAT ACC GGG	151
Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr Gly	
20 25 30	
CTC CTC GCG GAC GCT GCG CTC CTC TCA GAT ACT GTG CGC CCC ACA AAT	199
Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr Asn	
35 40 45	
GCC GCG CTC CCC ACG GAT GCT GCC TAC CCT GCG GTT AAT GTT CGG GAT	247
Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg Asp	
50 55 60 65	
CGC GAG GCC GCG TGG CCG CCT GCA CTG AAC TTC TGT TCC CGC CAC CCA	295
Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His Pro	
70 75 80	
AAG CTC TAT GGC CTA GTC GCT TTG GTT TTG CTG CTT CTG ATC GCC GCC	343
Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Leu Ile Ala Ala	
85 90 95	
TGT GTT CCT ATC TTC ACC CGC ACC GAG CCT CGG CCA GCG CTC ACA ATC	391
Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr Ile	
100 105 110	
ACC ACC TCG CCC AAC CTG GGT ACC CGA GAG AAT AAT GCA GAC CAG GTC	439
Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln Val	
115 120 125	
ACC CCT GTT TCC CAC ATT GGC TGC CCC AAC ACT ACA CAA CAG GGC TCT	487
Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly Ser	
130 135 140 145	
CCT GTG TTC GCC AAG CTA CTG GCT AAA AAC CAA GCA TCG TTG TGC AAT	535
Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys Asn	
150 155 160	
ACA ACT CTG AAC TGG CAC AGC CAA GAT GGA GCT GGG AGC TCA TAC CTA	583
Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr Leu	
165 170 175	
TCT CAA GGT CTG AGG TAC GAA GAA GAC AAA AAG GAG TTG GTG GTA GAC	631
Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val Asp	
180 185 190	

AGT CCC GGG CTC TAC TAC GTA TTT TTG GAA CTG AAG CTC AGT CCA ACA	679
Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro Thr	
195 200 205	
TTC ACA AAC ACA GGC CAC AAG GTG CAG GGC TGG GTC TCT CTT GTT TTG	727
Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val Leu	
210 215 220 225	
CAA GCA AAG CCT CAG GTA GAT GAC TTT GAC AAC TTG GCC CTG ACA GTG	775
Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr Val	
230 235 240	
GAA CTG TTC CCT TGC TCC ATG GAG AAC AAG TTA GTG GAC CGT TCC TGG	823
Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser Trp	
245 250 255	
AGT CAA CTG TTG CTC CTG AAG GCT GGC CAC CGC CTC AGT GTG GGT CTG	871
Ser Gln Leu Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly Leu	
260 265 270	
AGG GCT TAT CTG CAT GGA GCC CAG GAT GCA TAC AGA GAC TGG GAG CTG	919
Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu Leu	
275 280 285	
TCT TAT CCC AAC ACC ACC AGC TTT GGA CTC TTT CTT GTG AAA CCC GAC	967
Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro Asp	
290 295 300 305	
AAC CCA TGG GAA TGAGAACTAT CCTTCTTGTG ACTCCTAGTT GCTAAGTCCT	1019
Asn Pro Trp Glu	
CAAGCTGCTA TGTTTTATGG GGTCTGAGCA GGGGTCCCTT CCATGACTTT CTCTTGTCTT	1079
TAACTGGACT TGGTATTTAT TCTGAGCATA GCTCAGACAA GACTTTATAT AATTCAGTAG	1139
ATAGCATTAG TAAACTGCTG GGCAGCTGCT AGATAAAAAA AAATTTCTAA ATCAAAGTTT	1199
ATATTTATAT TAATATATAA AAATAAATGT GTTTGTAAAT AAAAAAAAAA AAAAA	1254

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: *Protein*

Met Asp Gln His Thr Leu Asp Val Glu Asp Thr Ala Asp Ala Arg His	
1 5 10 15	
Pro Ala Gly Thr Ser Cys Pro Ser Asp Ala Ala Leu Leu Arg Asp Thr	
20 25 30	
Gly Leu Leu Ala Asp Ala Ala Leu Leu Ser Asp Thr Val Arg Pro Thr	
35 40 45	

Asn Ala Ala Leu Pro Thr Asp Ala Ala Tyr Pro Ala Val Asn Val Arg  
 50 55 60  
 Asp Arg Glu Ala Ala Trp Pro Pro Ala Leu Asn Phe Cys Ser Arg His  
 65 70 75 80  
 Pro Lys Leu Tyr Gly Leu Val Ala Leu Val Leu Leu Leu Ile Ala  
 85 90 95  
 Ala Cys Val Pro Ile Phe Thr Arg Thr Glu Pro Arg Pro Ala Leu Thr  
 100 105 110  
 Ile Thr Thr Ser Pro Asn Leu Gly Thr Arg Glu Asn Asn Ala Asp Gln  
 115 120 125  
 Val Thr Pro Val Ser His Ile Gly Cys Pro Asn Thr Thr Gln Gln Gly  
 130 135 140  
 Ser Pro Val Phe Ala Lys Leu Leu Ala Lys Asn Gln Ala Ser Leu Cys  
 145 150 155 160  
 Asn Thr Thr Leu Asn Trp His Ser Gln Asp Gly Ala Gly Ser Ser Tyr  
 165 170 175  
 Leu Ser Gln Gly Leu Arg Tyr Glu Glu Asp Lys Lys Glu Leu Val Val  
 180 185 190  
 Asp Ser Pro Gly Leu Tyr Tyr Val Phe Leu Glu Leu Lys Leu Ser Pro  
 195 200 205  
 Thr Phe Thr Asn Thr Gly His Lys Val Gln Gly Trp Val Ser Leu Val  
 210 215 220  
 Leu Gln Ala Lys Pro Gln Val Asp Asp Phe Asp Asn Leu Ala Leu Thr  
 225 230 235 240  
 Val Glu Leu Phe Pro Cys Ser Met Glu Asn Lys Leu Val Asp Arg Ser  
 245 250 255  
 Trp Ser Gln Leu Leu Leu Lys Ala Gly His Arg Leu Ser Val Gly  
 260 265 270  
 Leu Arg Ala Tyr Leu His Gly Ala Gln Asp Ala Tyr Arg Asp Trp Glu  
 275 280 285  
 Leu Ser Tyr Pro Asn Thr Thr Ser Phe Gly Leu Phe Leu Val Lys Pro  
 290 295 300  
 Asp Asn Pro Trp Glu  
 305

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: human 4-1BB-L(7A)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 4..765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: *human, L*

GTC	ATG	GAA	TAC	GCC	TCT	GAC	GCT	TCA	CTG	GAC	CCC	GAA	GCC	CCG	TGG	48
Met	Glu	Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp		
1				5				10						15		
CCT	CCC	GCG	CCC	CGC	GCT	CGC	GCC	TGC	CGC	GTA	CTG	CCT	TGG	GCC	CTG	96
Pro	Pro	Ala	Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	
			20					25						30		
GTC	GCG	GGG	CTG	CTG	CTG	CTG	CTG	CTC	GCT	GCC	GCC	TGC	GCC	GTC		144
Val	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Ala	Cys	Ala	Val		
			35				40					45				
TTC	CTC	GCC	TGC	CCC	TGG	GCC	GTG	TCC	GGG	GCT	CGC	GCC	TCG	CCC	GGC	192
Phe	Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	
		50					55				60					
TCC	GCG	GCC	AGC	CCG	AGA	CTC	CGC	GAG	GGT	CCC	GAG	CTT	TCG	CCC	GAC	240
Ser	Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	
		65				70					75					
GAT	CCC	GCC	GGC	CTC	TTG	GAC	CTG	CGG	CAG	GGC	ATG	TTT	GCG	CAG	CTG	288
Asp	Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	
80				85				90						95		
GTG	GCC	CAA	AAT	GTT	CTG	CTG	ATC	GAT	GGG	CCC	CTG	AGC	TGG	TAC	AGT	336
Val	Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	
			100					105						110		
GAC	CCA	GGC	CTG	GCA	GGC	GTG	TCC	CTG	ACG	GGG	GGC	CTG	AGC	TAC	AAA	384
Asp	Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	
			115					120					125			
GAG	GAC	ACG	AAG	GAG	CTG	GTG	GTG	GCC	AAG	GCT	GGA	GTC	TAC	TAT	GTC	432
Glu	Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	
			130				135					140				
TTC	TTT	CAA	CTA	GAG	CTG	CGG	CGC	GTG	GTG	GCC	GGC	GAG	GGC	TCA	GGC	480
Phe	Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	
		145				150					155					
TCC	GTT	TCA	CTT	GCG	CTG	CAC	CTG	CAG	CCA	CTG	CGC	TCT	GCT	GCT	GGG	528
Ser	Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	
160					165					170					175	

GCC GCC GCC CTG GCT TTG ACC GTG GAC CTG CCA CCC GCC TCC TCC GAG Ala Ala Ala Leu Ala Leu Thr Val Asp Leu Pro Pro Ala Ser Ser Glu 180 185 190	576
GCT CGG AAC TCG GCC TTC GGT TTC CAG GGC CGC TTG CTG CAC CTG AGT Ala Arg Asn Ser Ala Phe Gly Phe Gln Gly Arg Leu Leu His Leu Ser 195 200 205	624
GCC GGC CAG CGC CTG GGC GTC CAT CTT CAC ACT GAG GCC AGG GCA CGC Ala Gly Gln Arg Leu Gly Val His Leu His Thr Glu Ala Arg Ala Arg 210 215 220	672
CAT GCC TGG CAG CTT ACC CAG GGC GCC ACA GTC TTG GGA CTC TTC CGG His Ala Trp Gln Leu Thr Gln Gly Ala Thr Val Leu Gly Leu Phe Arg 225 230 235	720
GTG ACC CCC GAA ATC CCA GCC GGA CTC CCT TCA CCG AGG TCG GAA Val Thr Pro Glu Ile Pro Ala Gly Leu Pro Ser Pro Arg Ser Glu 240 245 250	765
AACGCCCAGC CTGGGTGCAG CCCACCTGGA CAGAGTCCGA ATCCTACTCC ATCCTTCATG	826
GAGACCCCTG GTGCTGGGTC CCTGCTGCTT TCTCTACCTC AAGGGGCTTG GCAGGGGTCC	886
CTGCTGCTGA CCTCCCCTTG AGGACCCTCC TCACCCACTC CTTCCCCAAG TTGGACCTTG	946
ATATTTATTC TGAGCCTGAG CTCAGATAAT ATATTATATA TATTATATAT ATATATATAT	1006
TTCTATTTAA AGAGGATCCT GAGTTTGTGA ATGGACTTTT TTAGAGGAGT TGTTTTGGGG	1066
GGGGGGTCTT CGACATTGCC GAGGCTGGTC TTGAACTCCT GGACTTAGAC GATCCTCCTG	1126
CCTCAGCCTC CCAAGCAACT GGGATTCATC CTTTCTATTA ATTCATTGTA CTTATTTGCC	1186
TATTTGTGTG TATTGAGCAT CTGTAATGTG CCAGCATTGT GCCCAGGCTA GGGGGCTATA	1246
GAAACATCTA GAAATAGACT GAAAGAAAAT CTGAGTTATG GTAATACGTG AGGAATTTAA	1306
AGACTCATCC CCAGCCTCCA CCTCCTGTGT GATACTTGGG GGCTAGCTTT TTTCTTTCTT	1366
TCTTTTTTTT GAGATGGTCT TGTTCTGTCA ACCAGGCTAG AATGCAGCGG TGCAATCATG	1426
AGTCAATGCA GCCTCCAGCC TCGACCTCCC GAGGCTCAGG TGATCCTCCC ATCTCAGCCT	1486
CTCGAGTAGC TGGGACCACA GTTGTGTGCC ACCACACTTG GCTAACTTTT TAAATTTTTT	1546
GCGGAGACGG TATTGCTATG TTGCCAAGGT TGTTTACATG CCAGTACAAT TTATAATAAA	1606
CACTCATTTT TCC	1619

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: *human, L*

Met	Glu	Tyr	Ala	Ser	Asp	Ala	Ser	Leu	Asp	Pro	Glu	Ala	Pro	Trp	Pro	1	5	10	15
Pro	Ala	Pro	Arg	Ala	Arg	Ala	Cys	Arg	Val	Leu	Pro	Trp	Ala	Leu	Val	20	25	30	
Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Cys	Ala	Val	Phe	35	40	45		
Leu	Ala	Cys	Pro	Trp	Ala	Val	Ser	Gly	Ala	Arg	Ala	Ser	Pro	Gly	Ser	50	55	60	
Ala	Ala	Ser	Pro	Arg	Leu	Arg	Glu	Gly	Pro	Glu	Leu	Ser	Pro	Asp	Asp	65	70	75	80
Pro	Ala	Gly	Leu	Leu	Asp	Leu	Arg	Gln	Gly	Met	Phe	Ala	Gln	Leu	Val	85	90	95	
Ala	Gln	Asn	Val	Leu	Leu	Ile	Asp	Gly	Pro	Leu	Ser	Trp	Tyr	Ser	Asp	100	105	110	
Pro	Gly	Leu	Ala	Gly	Val	Ser	Leu	Thr	Gly	Gly	Leu	Ser	Tyr	Lys	Glu	115	120	125	
Asp	Thr	Lys	Glu	Leu	Val	Val	Ala	Lys	Ala	Gly	Val	Tyr	Tyr	Val	Phe	130	135	140	
Phe	Gln	Leu	Glu	Leu	Arg	Arg	Val	Val	Ala	Gly	Glu	Gly	Ser	Gly	Ser	145	150	155	160
Val	Ser	Leu	Ala	Leu	His	Leu	Gln	Pro	Leu	Arg	Ser	Ala	Ala	Gly	Ala	165	170	175	
Ala	Ala	Leu	Ala	Leu	Thr	Val	Asp	Leu	Pro	Pro	Ala	Ser	Ser	Glu	Ala	180	185	190	
Arg	Asn	Ser	Ala	Phe	Gly	Phe	Gln	Gly	Arg	Leu	Leu	His	Leu	Ser	Ala	195	200	205	
Gly	Gln	Arg	Leu	Gly	Val	His	Leu	His	Thr	Glu	Ala	Arg	Ala	Arg	His	210	215	220	
Ala	Trp	Gln	Leu	Thr	Gln	Gly	Ala	Thr	Val	Leu	Gly	Leu	Phe	Arg	Val	225	230	235	240
Thr	Pro	Glu	Ile	Pro	Ala	Gly	Leu	Pro	Ser	Pro	Arg	Ser	Glu	245	250				

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 768 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: mu4-1BB

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..768

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 70..768

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG	48
Met Gly Asn Asn Cys Tyr Asn Val Val Ile Val Leu Leu Leu Val	
-23 -20 -15 -10	
GGC TGT GAG AAG GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TGT CAG	96
Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln	
-5 1 5	
CCT GGT ACT TTC TGC AGA AAA TAC AAT CCA GTC TGC AAG AGC TGC CCT	144
Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro	
10 15 20 25	
CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC TGT AAC ATC TGC	192
Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys	
30 35 40	
AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC	240
Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr	
45 50 55	
CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA	288
His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro	
60 65 70	
CAG TGC ACC AGA TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG	336
Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr	
75 80 85	
AAG CAG GGT TGC AAA ACC TGT AGC TTG GGA ACA TTT AAT GAC CAG AAC	384
Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn	
90 95 100 105	
GGT ACT GGC GTC TGT CGA CCC TGG ACG AAC TGC TCT CTA GAC GGA AGG	432
Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg	
110 115 120	



TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC	480
Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro	
125 130 135	
CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG	528
Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu	
140 145 150	
GGA GGA CCA GGA GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG	576
Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala	
155 160 165	
CTG ACA TCG GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC	624
Leu Thr Ser Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe	
170 175 180 185	
TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC ATA TTC AAG CAA	672
Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln	
190 195 200	
CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC	720
Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser	
205 210 215	
TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGA GGC TAT GAG CTG	768
Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Tyr Glu Leu	
220 225 230	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val	
-23 -20 -15 -10	
Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln	
-5 1 5	
Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro	
10 15 20 25	
Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys	
30 35 40	
Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr	
45 50 55	
His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro	
60 65 70	
Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr	
75 80 85	

Lys	Gln	Gly	Cys	Lys	Thr	Cys	Ser	Leu	Gly	Thr	Phe	Asn	Asp	Gln	Asn		
90					95					100					105		
Gly	Thr	Gly	Val	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Ser	Leu	Asp	Gly	Arg		
				110					115					120			
Ser	Val	Leu	Lys	Thr	Gly	Thr	Thr	Glu	Lys	Asp	Val	Val	Cys	Gly	Pro		
			125					130					135				
Pro	Val	Val	Ser	Phe	Ser	Pro	Ser	Thr	Thr	Ile	Ser	Val	Thr	Pro	Glu		
			140				145					150					
Gly	Gly	Pro	Gly	Gly	His	Ser	Leu	Gln	Val	Leu	Thr	Leu	Phe	Leu	Ala		
	155					160					165						
Leu	Thr	Ser	Ala	Leu	Leu	Leu	Ala	Leu	Ile	Phe	Ile	Thr	Leu	Leu	Phe		
170					175					180					185		
Ser	Val	Leu	Lys	Trp	Ile	Arg	Lys	Lys	Phe	Pro	His	Ile	Phe	Lys	Gln		
			190						195					200			
Pro	Phe	Lys	Lys	Thr	Thr	Gly	Ala	Ala	Gln	Glu	Glu	Asp	Ala	Cys	Ser		
			205					210					215				
Cys	Arg	Cys	Pro	Gln	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Gly	Tyr	Glu	Leu		
		220					225					230					

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1415 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: hu4-1BE
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 120..887
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 189..884
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 120..188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGTGGAAAAGT TCTCCGGCAG CCCTGAGATC TCAAGAGTGA CATTGTGAG ACCAGCTAAT	60
TTGATTAAAA TTCTCTTGA ATCAGCTTTG CTAGTATCAT ACCTGTGCCA GATTTTCATC	119
ATG GGA AAC AGC TGT TAC AAC ATA GTA GCC ACT CTG TTG CTG GTC CTC Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu -23 -20 -15 -10	167
AAC TTT GAG AGG ACA AGA TCA TTG CAG GAT CCT TGT AGT AAC TGC CCA Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro -5 1 5	215
GCT GGT ACA TTC TGT GAT AAT AAC AGG AAT CAG ATT TGC AGT CCC TGT Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys 10 15 20 25	263
CCT CCA AAT AGT TTC TCC AGC GCA GGT GGA CAA AGG ACC TGT GAC ATA Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile 30 35 - 40	311
TGC AGG CAG TGT AAA GGT GTT TTC AGG ACC AGG AAG GAG TGT TCC TCC Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser 45 50 55	359
ACC AGC AAT GCA GAG TGT GAC TGC ACT CCA GGG TTT CAC TGC CTG GGG Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly 60 65 70	407
GCA GGA TGC AGC ATG TGT GAA CAG GAT TGT AAA CAA GGT CAA GAA CTG Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu 75 80 85	455
ACA AAA AAA GGT TGT AAA GAC TGT TGC TTT GGG ACA TTT AAC GAT CAG Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln 90 95 100 105	503
AAA CGT GGC ATC TGT CGA CCC TGG ACA AAC TGT TCT TTG GAT GGA AAG Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys 110 115 120	551
TCT GTG CTT GTG AAT GGG ACG AAG GAG AGG GAC GTG GTC TGT GGA CCA Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro 125 130 135	599
TCT CCA GCC GAC CTC TCT CCG GGA GCA TCC TCT GTG ACC CCG CCT GCC Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala 140 145 150	647
CCT GCG AGA GAG CCA GGA CAC TCT CCG CAG ATC ATC TCC TTC TTT CTT Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu 155 160 165	695
GCG CTG ACG TCG ACT GCG TTG CTC TTC CTG CTG TTC TTC CTC ACG CTC Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Phe Phe Leu Thr Leu 170 175 180 185	743

CGT TTC TCT GTT GTT AAA CGG GGC AGA AAG AAA CTC CTG TAT ATA TTC	791
Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe	
190 195 200	
AAA CAA CCA TTT ATG AGA CCA GTA CAA ACT ACT CAA GAG GAA GAT GGC	839
Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly	
205 210 215	
TGT AGC TGC CGA TTT CCA GAA GAA GAA GAA GGA GGA TGT GAA CTG TGAAATGGAA	
894	
Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu	
220 225 230	
GTCAATAGGG CTGTTGGGAC TTTCTTGAAA AGAAGCAAGG AAATATGAGT CATCCGCTAT	954
CACAGCTTTC AAAAGCAAGA ACACCATCCT ACATAATACC CAGGATTCCC CCAACACACG	1014
TTCTTTTCTA AATGCCAATG AGTTGGCCTT TAAAAATGCA CCACTTTTTTT TTTTTTTTTT	1074
GACAGGGTCT CACTCTGTCA CCCAGGCTGG AGTGCAGTGG CACCACCATG GCTCTCTGCA	1134
GCCTTGACCT CTGGGAGCTC AAGTGATCCT CCTGCCTCAG TCTCCTAGTA GCTGGA ACTA	1194
CAAGGAAGGG CCACCACACC TGACTAACTT TTTTGTTTTT TGTTTGGTAA AGATGGCATT	1254
TCGCCATGTT GTACAGGCTG GTCTCAA ACT CCTAGGTTCA CTTTGGCCTC CCAAAGTGCT	1314
GGGATTACAG ACATGAACTG CCAGGCCCGG CCAAATAAT GCACCACTTT TAACAGAACA	1374
GACAGATGAG GACAGAGCTG GTGATAAAAA AAAAAAAAAA A	1415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu	
-23 -20 -15 -10	
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro	
-5 1 5	
Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys	
10 15 20 25	
Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile	
30 35 40	
Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser	
45 50 55	
Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly	
60 65 70	



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CACAAGATCT GGGCTCCTCT GGAGTCACAG AAATG  
35

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGACTAGTT CACTCTGGAG TCACAGAAAT G  
31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 34 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATAGCGGCCG CTGCCAGATT TCATCATGGG AAAC  
34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 40 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACAAGATCTG GGCTCCTGCG GAGAGTGTCC TGGCTCTCTC  
40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: hIgG1Fc

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

G GTA CCG CTA GCG TCG ACA GGC CTA GGA TAT CGA TAC GTA GAG CCC	46
Val Pro Leu Ala Ser Thr Gly Leu Gly Tyr Arg Tyr Val Glu Pro	
1 5 10 15	
AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA	94
Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	
20 25 30	
CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC	142
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	
35 40 45	
ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC	190
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	
50 55 60	
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC	238
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly	
65 70 75	
GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC	286
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	
80 85 90 95	
AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG	334
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	
100 105 110	
CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA	382
Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
115 120 125	
GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA	430
Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
130 135 140	

CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC	478
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
145 150 155	
CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC	526
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile	
160 165 170 175	
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC	574
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
180 185 190	
ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG	622
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
195 200 205	
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC	670
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
210 215 220	
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC	718
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
225 230 235	
TCC CTG TCT CCG GGT AAA TGAAGTAGT	745
Ser Leu Ser Pro Gly Lys	
240 245	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Pro Leu Ala Ser Thr Gly Leu Gly Tyr Arg Tyr Val Glu Pro Arg	
1 5 10 15	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu	
20 25 30	
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr	
35 40 45	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val	
50 55 60	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val	
65 70 75 80	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser	
85 90 95	



Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	100	105	110	
Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	115	120	125	
Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	130	135	140	
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	145	150	155	160
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg	His	Ile	Ala	165	170	175	
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	180	185	190	
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	195	200	205	
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	210	215	220	
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	225	230	235	240
Leu	Ser	Pro	Gly	Lys												245			